

#5

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/53/973
Source: PCT
Date Processed by STIC: 5/10/5

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PCT

RAW SEQUENCE LISTING

DATE: 05/10/2005

PATENT APPLICATION: US/10/531,973

TIME: 13:51:41

Input Set : A:\14875-142US1.txt

Output Set: N:\CRF4\05102005\J531973.raw

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3 <110> APPLICANT: Kitamura, Toshio
4     Kumagai, Hidetoshi
6 <120> TITLE OF INVENTION: MAST CELL-DERIVED MEMBRANE PROTEINS
8 <130> FILE REFERENCE: 14875-142US1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/531,973
C--> 10 <141> CURRENT FILING DATE: 2005-04-28
10 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/013921
11 <151> PRIOR FILING DATE: 2003-10-30
13 <150> PRIOR APPLICATION NUMBER: JP 2002-316680
14 <151> PRIOR FILING DATE: 2002-10-30
16 <150> PRIOR APPLICATION NUMBER: JP 2002-354165
17 <151> PRIOR FILING DATE: 2002-12-05
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1752
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (148)..(1104)
33 <400> SEQUENCE: 1
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36 gtctcagaga ctggccgtcc cctagcggga ctgaaccgtg gacggtccag ccgtggcctg      120
38 cctgcccgtg acccgtgtgt gggagaa atg acc caa ctg gcc tca gct gtg tgg      174
39                               Met Thr Gln Leu Ala Ser Ala Val Trp
40                               1                               5
42 ctg ccc acg ctg ttg ctg ctg ctg ctg ctt ttt tgg ctt cca ggc tgt      222
43 Leu Pro Thr Leu Leu Leu Leu Leu Leu Phe Trp Leu Pro Gly Cys
44 10                               15                               20                               25
46 gtc cct ctg cat ggt ccc agc acc atg aca gga agt gtg ggt caa tcc      270
47 Val Pro Leu His Gly Pro Ser Thr Met Thr Gly Ser Val Gly Gln Ser
48                               30                               35                               40
50 ctg agt gtg tcg tgt cag tat gag gag aaa ttt aag act aag gac aaa      318
51 Leu Ser Val Ser Cys Gln Tyr Glu Glu Lys Phe Lys Thr Lys Asp Lys
52                               45                               50                               55
54 tac tgg tgc aga ggg tca ctt aag gta ctg tgc aaa gat att gtc aag      366
55 Tyr Trp Cys Arg Gly Ser Leu Lys Val Leu Cys Lys Asp Ile Val Lys
56                               60                               65                               70
58 acc agc agc tca gaa gaa gct agg agt ggc aga gtg acc atc agg gac      414
59 Thr Ser Ser Ser Glu Glu Ala Arg Ser Gly Arg Val Thr Ile Arg Asp
60                               75                               80                               85
62 cat cca gac aac ctc acc ttc aca gtg acc tat gag agc ctc acc ctg      462

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63	His	Pro	Asp	Asn	Leu	Thr	Phe	Thr	Val	Thr	Tyr	Glu	Ser	Leu	Thr	Leu	
64	90					95					100					105	
66	gat	gat	gca	gac	acc	tac	atg	tgt	gcg	gtg	gat	ata	cca	ttt	ttc	aat	510
67	Asp	Asp	Ala	Asp	Thr	Tyr	Met	Cys	Ala	Val	Asp	Ile	Pro	Phe	Phe	Asn	
68					110					115					120		
70	gcc	ccc	ttg	ggg	ctc	gat	aag	tac	ttc	aag	att	gaa	ttg	tct	gtg	gtt	558
71	Ala	Pro	Leu	Gly	Leu	Asp	Lys	Tyr	Phe	Lys	Ile	Glu	Leu	Ser	Val	Val	
72				125					130					135			
74	cca	agt	gag	gac	cca	gtt	tca	tct	cca	gga	cca	aca	cta	gag	aca	cct	606
75	Pro	Ser	Glu	Asp	Pro	Val	Ser	Ser	Pro	Gly	Pro	Thr	Leu	Glu	Thr	Pro	
76			140					145					150				
78	gtg	gtg	tcc	acc	agt	ctg	cct	acc	aag	ggg	ccc	gcc	cta	gga	tcc	aac	654
79	Val	Val	Ser	Thr	Ser	Leu	Pro	Thr	Lys	Gly	Pro	Ala	Leu	Gly	Ser	Asn	
80		155					160				165						
82	aca	gag	gac	cg	cgt	gag	cat	gac	tat	tcc	cag	ggc	ttg	agg	ctc	cca	702
83	Thr	Glu	Asp	Arg	Arg	Glu	His	Asp	Tyr	Ser	Gln	Gly	Leu	Arg	Leu	Pro	
84	170				175					180					185		
86	gcg	ctg	ttg	tct	gtg	tta	gct	ctc	ctg	ctg	ttt	ctg	ttg	gtg	ggg	aca	750
87	Ala	Leu	Leu	Ser	Val	Leu	Ala	Leu	Leu	Leu	Phe	Leu	Leu	Val	Gly	Thr	
88				190					195					200			
90	tct	ctg	ctg	gcc	tgg	agg	atg	ttc	cag	aag	cgg	ctg	gtc	aaa	gct	gat	798
91	Ser	Leu	Leu	Ala	Trp	Arg	Met	Phe	Gln	Lys	Arg	Leu	Val	Lys	Ala	Asp	
92			205					210					215				
94	agg	cat	cca	gag	ctg	tcc	cag	aac	ctc	aga	cag	gct	tct	gag	cag	aat	846
95	Arg	His	Pro	Glu	Leu	Ser	Gln	Asn	Leu	Arg	Gln	Ala	Ser	Glu	Gln	Asn	
96			220				225				230						
98	gag	tgc	cag	tat	gtg	aat	ttg	cag	ctg	cac	acg	tgg	tct	ctg	agg	gaa	894
99	Glu	Cys	Gln	Tyr	Val	Asn	Leu	Gln	Leu	His	Thr	Trp	Ser	Leu	Arg	Glu	
100		235				240					245						
102	gag	ccg	gtg	cta	cca	agt	cag	gta	gaa	gtg	gtg	gaa	tat	agc	aca	ttg	942
103	Glu	Pro	Val	Leu	Pro	Ser	Gln	Val	Glu	Val	Glu	Tyr	Ser	Thr	Leu		
104	250				255				260					265			
106	gca	tta	ccc	cag	gaa	gag	ctt	cac	tat	tca	tcc	gtg	gca	ttc	aac	tcc	990
107	Ala	Leu	Pro	Gln	Glu	Glu	Leu	His	Tyr	Ser	Ser	Val	Ala	Phe	Asn	Ser	
108				270				275					280				
110	cag	agg	cag	gat	tct	cac	gcc	aat	gga	gat	tct	ctt	cat	caa	cct	cag	1038
111	Gln	Arg	Gln	Asp	Ser	His	Ala	Asn	Gly	Asp	Ser	Leu	His	Gln	Pro	Gln	
112			285					290				295					
114	gac	cag	aaa	gca	gag	tac	agt	gag	atc	cag	aag	ccc	aga	aaa	gga	ctc	1086
115	Asp	Gln	Lys	Ala	Glu	Tyr	Ser	Glu	Ile	Gln	Lys	Pro	Arg	Lys	Gly	Leu	
116		300					305				310						
118	tct	gac	ctt	tac	ctg	tga	ctc	ctt	gtc	cca	ctg	atc	cct	gag	ggt	gga	1134
119	Ser	Asp	Leu	Tyr	Leu												
120		315															
122	ctaccaggtt	ccaaggtcc	ctgctggctg	ctgccctcaa	tgatcatgagc	ctcagtggtc											1194
124	tcactaaaga	tgagcaggag	ccagggtctc	gtgggcacag	tctcatccca	ctggctctct											1254
126	cctcttagcc	tgtattttgt	tctgcctctg	gggtgtggaag	acatcgatgc	tgctcttttg											1314
128	gggctctggg	aattgacatg	gttcgtatag	aacggtactt	gtgttagtta	gctttgtagt											1374
130	gtcagtcacg	gaagaacatc	tgtgggtcact	gggaaagtgg	gggacccatg	agactacaaa											1434

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132 ggaaggggag tcatggaggt actaaacacc aactccttca tctcacagag aaaaaaacct 1494
134 aagctctgag gacaaaagcc tggcccgtag caccaaggctc aggggcaaat tcctctggac 1554
136 tcatttttat ttttattttt tgttttttga gacaggggtct ctctgtgtag ctttggtgt 1614
138 cctggaactc actctgtaaa ccagaatggc ctcagactca caaagatctg cctgcctctg 1674
140 cctccaaagg tgtgtgccac aatgcctggc ttctctgaat tcttaagtaa aagatgaaat 1734
142 aaagtttata atatcttt 1752
145 <210> SEQ ID NO: 2
146 <211> LENGTH: 318
147 <212> TYPE: PRT
148 <213> ORGANISM: Mus musculus
150 <400> SEQUENCE: 2
151 Met Thr Gln Leu Ala Ser Ala Val Trp Leu Pro Thr Leu Leu Leu Leu
152 1 5 10 15
154 Leu Leu Leu Phe Trp Leu Pro Gly Cys Val Pro Leu His Gly Pro Ser
155 20 25 30
157 Thr Met Thr Gly Ser Val Gly Gln Ser Leu Ser Val Ser Cys Gln Tyr
158 35 40 45
160 Glu Glu Lys Phe Lys Thr Lys Asp Lys Tyr Trp Cys Arg Gly Ser Leu
161 50 55 60
163 Lys Val Leu Cys Lys Asp Ile Val Lys Thr Ser Ser Ser Glu Glu Ala
164 65 70 75 80
166 Arg Ser Gly Arg Val Thr Ile Arg Asp His Pro Asp Asn Leu Thr Phe
167 85 90 95
169 Thr Val Thr Tyr Glu Ser Leu Thr Leu Asp Asp Ala Asp Thr Tyr Met
170 100 105 110
172 Cys Ala Val Asp Ile Pro Phe Phe Asn Ala Pro Leu Gly Leu Asp Lys
173 115 120 125
175 Tyr Phe Lys Ile Glu Leu Ser Val Val Pro Ser Glu Asp Pro Val Ser
176 130 135 140
178 Ser Pro Gly Pro Thr Leu Glu Thr Pro Val Val Ser Thr Ser Leu Pro
179 145 150 155 160
181 Thr Lys Gly Pro Ala Leu Gly Ser Asn Thr Glu Asp Arg Arg Glu His
182 165 170 175
184 Asp Tyr Ser Gln Gly Leu Arg Leu Pro Ala Leu Leu Ser Val Leu Ala
185 180 185 190
187 Leu Leu Leu Phe Leu Leu Val Gly Thr Ser Leu Leu Ala Trp Arg Met
188 195 200 205
190 Phe Gln Lys Arg Leu Val Lys Ala Asp Arg His Pro Glu Leu Ser Gln
191 210 215 220
193 Asn Leu Arg Gln Ala Ser Glu Gln Asn Glu Cys Gln Tyr Val Asn Leu
194 225 230 235 240
196 Gln Leu His Thr Trp Ser Leu Arg Glu Glu Pro Val Leu Pro Ser Gln
197 245 250 255
199 Val Glu Val Val Glu Tyr Ser Thr Leu Ala Leu Pro Gln Glu Glu Leu
200 260 265 270
202 His Tyr Ser Ser Val Ala Phe Asn Ser Gln Arg Gln Asp Ser His Ala
203 275 280 285
205 Asn Gly Asp Ser Leu His Gln Pro Gln Asp Gln Lys Ala Glu Tyr Ser
206 290 295 300

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208 Glu Ile Gln Lys Pro Arg Lys Gly Leu Ser Asp Leu Tyr Leu
209 305                      310                      315
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 687
214 <212> TYPE: DNA
215 <213> ORGANISM: Mus musculus
217 <220> FEATURE:
218 <221> NAME/KEY: CDS
219 <222> LOCATION: (1)..(687)
222 <400> SEQUENCE: 3
223 atg att ccc aga gta ata aga ttg tgg ctg cct tca gct ctg ttc ctc      48
224 Met Ile Pro Arg Val Ile Arg Leu Trp Leu Pro Ser Ala Leu Phe Leu
225 1                      5                      10                      15
227 tct cag gtc cca ggc tgt gtc cca ctg cat ggc ccc agc act atc aca      96
228 Ser Gln Val Pro Gly Cys Val Pro Leu His Gly Pro Ser Thr Ile Thr
229                      20                      25                      30
231 ggc gct gtt ggg gaa tcg ctc agt gtg tca tgt caa tac gag gag aaa      144
232 Gly Ala Val Gly Glu Ser Leu Ser Val Ser Cys Gln Tyr Glu Glu Lys
233                      35                      40                      45
235 ttc aag act aag gac aaa ttc tgg tgc aga ggg tca ctg aag gta ctc      192
236 Phe Lys Thr Lys Asp Lys Phe Trp Cys Arg Gly Ser Leu Lys Val Leu
237                      50                      55                      60
239 tgt aaa gat att gtc aag acc agc agc tca gaa gaa gtt agg aat ggc      240
240 Cys Lys Asp Ile Val Lys Thr Ser Ser Ser Glu Glu Val Arg Asn Gly
241 65                      70                      75                      80
243 cga gtg acc atc agg gac cat cca gac aac ctc acc ttc aca gtg acc      288
244 Arg Val Thr Ile Arg Asp His Pro Asp Asn Leu Thr Phe Thr Val Thr
245                      85                      90                      95
247 tat gag agc ctc acc ctg gag gat gca gac acc tac atg tgt gcg gtg      336
248 Tyr Glu Ser Leu Thr Leu Glu Asp Ala Asp Thr Tyr Met Cys Ala Val
249                      100                     105                     110
251 gat ata tca ctt ttt gat ggc tcc ttg ggg ttc gat aag tac ttc aag      384
252 Asp Ile Ser Leu Phe Asp Gly Ser Leu Gly Phe Asp Lys Tyr Phe Lys
253                      115                     120                     125
255 att gag ttg tct gtg gtt cca agt gag gac cca gtc aca ggt tcg agc      432
256 Ile Glu Leu Ser Val Val Pro Ser Glu Asp Pro Val Thr Gly Ser Ser
257                      130                     135                     140
259 ctt gag agt ggt aga gat atc ctg gaa tcc ccc aca tcc tca gtt ggg      480
260 Leu Glu Ser Gly Arg Asp Ile Leu Glu Ser Pro Thr Ser Ser Val Gly
261 145                      150                     155                     160
263 cac act cat ccc agt gtg acc aca gat gac aca att cct gct ccc tgc      528
264 His Thr His Pro Ser Val Thr Thr Asp Asp Thr Ile Pro Ala Pro Cys
265                      165                     170                     175
267 cct cag cct cgg tct ctt cgg agc agc ctc tac ttc tgg gtc ctg gtg      576
268 Pro Gln Pro Arg Ser Leu Arg Ser Ser Leu Tyr Phe Trp Val Leu Val
269                      180                     185                     190
271 tct ctg aag ttg ttc ctg ttc ctg agc atg ctt ggt gct gtc ctc tgg      624
272 Ser Leu Lys Leu Phe Leu Phe Leu Ser Met Leu Gly Ala Val Leu Trp
273                      195                     200                     205

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275 gtg aac agg cct cag agg tgc tct ggg gga agc agc act cag ccc tgt      672
276 Val Asn Arg Pro Gln Arg Cys Ser Gly Gly Ser Ser Thr Gln Pro Cys
277      210                      215                      220
279 tat gag aac cag tga      687
280 Tyr Glu Asn Gln
281 225
284 <210> SEQ ID NO: 4
285 <211> LENGTH: 228
286 <212> TYPE: PRT
287 <213> ORGANISM: Mus musculus
289 <400> SEQUENCE: 4
290 Met Ile Pro Arg Val Ile Arg Leu Trp Leu Pro Ser Ala Leu Phe Leu
291 1      5      10      15
293 Ser Gln Val Pro Gly Cys Val Pro Leu His Gly Pro Ser Thr Ile Thr
294      20      25      30
296 Gly Ala Val Gly Glu Ser Leu Ser Val Ser Cys Gln Tyr Glu Glu Lys
297      35      40      45
299 Phe Lys Thr Lys Asp Lys Phe Trp Cys Arg Gly Ser Leu Lys Val Leu
300      50      55      60
302 Cys Lys Asp Ile Val Lys Thr Ser Ser Ser Glu Glu Val Arg Asn Gly
303 65      70      75      80
305 Arg Val Thr Ile Arg Asp His Pro Asp Asn Leu Thr Phe Thr Val Thr
306      85      90      95
308 Tyr Glu Ser Leu Thr Leu Glu Asp Ala Asp Thr Tyr Met Cys Ala Val
309      100     105     110
311 Asp Ile Ser Leu Phe Asp Gly Ser Leu Gly Phe Asp Lys Tyr Phe Lys
312      115     120     125
314 Ile Glu Leu Ser Val Val Pro Ser Glu Asp Pro Val Thr Gly Ser Ser
315      130     135     140
317 Leu Glu Ser Gly Arg Asp Ile Leu Glu Ser Pro Thr Ser Ser Val Gly
318 145     150     155     160
320 His Thr His Pro Ser Val Thr Thr Asp Asp Thr Ile Pro Ala Pro Cys
321      165     170     175
323 Pro Gln Pro Arg Ser Leu Arg Ser Ser Leu Tyr Phe Trp Val Leu Val
324      180     185     190
326 Ser Leu Lys Leu Phe Leu Phe Leu Ser Met Leu Gly Ala Val Leu Trp
327      195     200     205
329 Val Asn Arg Pro Gln Arg Cys Ser Gly Gly Ser Ser Thr Gln Pro Cys
330      210     215     220
332 Tyr Glu Asn Gln
333 225
336 <210> SEQ ID NO: 5
337 <211> LENGTH: 19
338 <212> TYPE: DNA
339 <213> ORGANISM: Artificial
341 <220> FEATURE:
342 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
344 <400> SEQUENCE: 5
345 gggggtggac catcctcta

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/531,973

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Input Set : A:\14875-142US1.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date